

**Figures****Figure 1 A**

1 gtggcacttt tcggggaaat gtgcgcggaa ccctatttg tttatttttc taaatacatt  
61 caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa  
121 ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt  
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241 tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt  
301 ttgcgccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg  
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1081 atctcatgac caaaatccct taacgtgagt ttctgtcca ctgagcgtca gaccccgtag  
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1381 tcctgttacc agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa
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2101 tgtgtggaat tgtgagcgga taacaatttc acacaggaaa cagctatgac catgattacg
                                     KpnI
                                     -----
2161 ccaagcgcgc aattaaccct cactaaaggg aacaaaagct ggggtaccggg cccccctcg
      >>.....T3 .....>>
                                     HindIII
                                     -----
                                     PstI
                                     -----
2221 aggtcgacgg tatcgataag cttgatatcg aattcctgca gccccgaga cgcgtgttct
      >>.pSAG1.>
2281 aaccacaaac cttgagacgc gtgttccaac cagcaccct gacacgcgtg ttccaaccac
      >.....pSAG1.....>
2341 gcaccctgag acgcgtgttc tawccacgca ccctgagacg cgtgttctaa ccacgcaccc
      >.....pSAG1.....>

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2401 tgagacgcgt gttctgccgc acaatgtgca cctgtaggaa gctgtagtca ctgctgattc  
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2461 tcactgttct cggcaagggc cgacgaccgg agtacagttt ttgtgggcag agccgttggtg  
>.....pSAG1.....>

2521 cagctttccg ttcttctcgg ttgtgtcaca tgtgtcattg tcgtgtaaac acacggttgt  
>.....pSAG1.....>

2581 atgtcggttt cgctgcacca cttcattatt tcttctgggt ttttgacgag tatgcatgag  
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>>.....SAG1 CDS.....>>>  
>>>

2641 aaaaaaatca ctggatatac caccgttgat atatcccaat ggcacgtgaa agaacatttt  
>.....CAT CDS.....>

2701 gaggcatttc agtcagttgc tcaatgtacc tataaccaga ccgttcagct ggatattacg  
>.....CAT CDS.....>

2761 gcctttttta agaccgtaaa gaaaaataag cacaagtttt atccggcctt tattcacatt  
>.....CAT CDS.....>

2821 cttgcccgcc tgatgaatgc tcatccggaa ttccgtatgg caatgaaaga cggtagctg  
>.....CAT CDS.....>

2881 gtgatatggg atagtgttca cccttggtac accgttttcc atgagcaaac tgaaacgttt  
>.....CAT CDS.....>

2941 tcatcgtctt ggagtgaata ccacgacgat ttccggcagt ttctacacat atattcgaa  
>.....CAT CDS.....>

3001 gatgtggcgt gttacggtga aaacctggcc tatttccta aagggtttat tgagaatatg  
>.....CAT CDS.....>

3061 tttttcgtct cagccaatcc ctgggtgagt ttcaccagtt ttgatttaaa cgtggccaat  
>.....CAT CDS.....>

3121 atggacaact tcttcgcccc cgttttcacc atgggcaaatt attatacgca aggcgacaag  
>.....CAT CDS.....>

3181 gtgctgatgc cgctggcgat tcaggttcat catgccgttt gtgatggctt ccatgtcggc  
>.....CAT CDS.....>

3241 agaatgctta atgaattaca acagtactgc gatgagtggc agggcggggc ktaaktralc  
>.....CAT CDS.....>>>  
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3301 accgttggtg tcacttctca aatcgacaaa ggaaacacac ttcgtgcagc atgtgcccc  
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3361 ttataaagaa actgagttgt tccgctgtgg cttgcagggtg tcacatccac aaaaaccggc
>.....SAG1-I.....>

3421 cgactctaaa taggagtgtt tcgcagcaag cagcgaaagt ttatgactgg gtccgaatct
>.....SAG1-I.....>

3481 ctgaacggat gtgtggcgga cctggctgat gttgatcgcc gtcgacacac gcgccacatg
>.....SAG1-I.....>

3541 ggtcaatata caagacagct atcagttggt ttagtcgaac cggttaacac aattcttgcc
>.....SAG1-I.....>
      HindIII
      -----
3601 ccccgaaag cttcgaatct ctgaacggat gtgtggcgga cctggctgat gttgatcgcc
>....>>
      >>.....SAG1-II.....>

3661 gtcgacacac gcgccacatg ggtcaatata caagacagct atcagttggt ttagtcgaac
>.....SAG1-II.....>

3721 cggttaacac aattcttgcc ccccgaggg ggatccacta gttctagagc ggcctcgagg
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>.....vector.....>
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>.....pTUB1.....>

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>.....pTUB1.....>

3961 gtcattagat actgaatcag gtaacgatac atgagcagca tcctcgtggt ccaggcgcat
>.....pTUB1.....>

4021 gtcctgctcc ggcttgcaac caaggaccgg tggttcatct ttgggtctct ccgtactggg
>.....pTUB1.....>

4081 tggtagaggt gaaactgtcg acgtggatgc agctgccctg cttagagtac ggacgaagt
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4141 aatagctgcg tctgcatgaa caaggggctc tgaggccgcg tgtgatacga aaggtttgct
>.....pTUB1.....>

4201 ggctactgaa cataggtctc gcagtgcggg gccatactcc agtcggcctt cacgaaactt
>.....pTUB1.....>

4261 cgtgaccagg cgatcaacaa gcggcgtcac gcgagttaaa tccgtccaga gaaagccacc
>.....pTUB1.....>

4321 atagtgcacc atatactgcc ggcacatctt gctgaaagtc gtggcgtgtc gatcagctaa
>.....pTUB1.....>
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>.....pTUB1.....>

4441 cctagccacc gtttcaccag cgtccgatgc aggcacacct agccgatacc tgtgaccgtt  
>.....pTUB1.....>

4501 catatatgag ttgctattac atctgtcggc cgtaacgaca caaggagatg cggctggagg  
>.....pTUB1.....>

4561 caacggggtt gtgagcacca ttttgactct gtcacggagt aaaaaacatt tattcgaact  
>.....pTUB1.....>

4621 ttgtacgagc gcagtcagta gaagtcacac acgcgtatca actacgctgc aattacagag  
>.....pTUB1.....>

4681 gacagggaca gggaaaaaaa gccgaagagg ttgccgggtg taggagatga cgagacgttt  
>.....pTUB1.....>

4741 aaacggccgc tggctattgt tggggcatcg ttgagccaca agcgatcaag gtgaaaacaa  
>.....pTUB1.....>

4801 agttaaatag ttatgctgga gcgattgccc tgctgaatct tcagatcgga cgaacagtca  
>.....pTUB1.....>

4861 ttctggccca ctgtacttga tgtgttcgat gtaaatcaca ctacgctcgc tgctcggtag  
>.....pTUB1.....>

4921 caatcaagtt gctcttttct ctcttttcta gacacggtaa gaacgcttat gaacacgcatt  
>.....pTUB1.....>

4981 acacgcatag tttttgctag aatgcagcga ccagatgtcg caaggctcgc tcccccatcg  
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>.....pTUB1.....>

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>.....pTUB1.....>

5221 tgcattgaac ttctgaagtg cgtagtacct ggctcctaatt gctgttttgt gtttcgctgt  
>.....pTUB1.....>

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>.....pTUB1.....>

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>.....pTUB1.....>

5581 tcgtcatagt aactcagcgc ccccttgccc cccccagca gtgagatgca agacaatcct  
>.....pTUB1.....>

5641 ctctaccaca gcttttgttg cgtctgtttc aaattttcag cgctcgcgaa aggcacacg  
>.....pTUB1.....>

5701 aacaacatta tgagaggag caggtttgtg gggctggcgg gtgcaggaat gtgttcctgc  
>.....pTUB1.....>

5761 gaaaaaggcc tctgctgaga aggtcgtggc gtttgaaaaa tatccgaggt agcaaagact  
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5821 tgtttcagtg ctcccctttt gaagacctgc ggcggcagtg cactgaagag taactccaaa  
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>.....pTUB1.....>

5941 tcgtcacaga ccacgaaaaa cgaaccatcg aagacgatca ctgcgtccgc gtgcatctgg  
>.....pTUB1.....>

6001 atggatgacc cacatctgtt gcagccgtcg cagacatgca tgtcccgcgt tcgtgaaatt  
>.....pTUB1.....>

6061 ctctgcatca gcggagtgat caggaatcat cgtctcagcg ggatgacgtt gcggagcagg  
>.....pTUB1.....>

6121 ccggctcgcg ggggcagtca gatgccgaag gcgtaactca ggacgcttgc gctcatcgca  
>.....pTUB1.....>

6181 gaacaggggt ggtgcctgca ttgggtgcgg ttggtgatcc tggttggacc ggtggagatg  
>.....pTUB1.....>

6241 cgcgcgcacg aaggggatgt gtcagaaaca ttttgtttgt tctctgtgaa cttttagatg  
>.....pTUB1.....>

6301 tgttaaaggc ggcgaatatt agcagagagt cctccttgtt ggattctctc ttgaatttcg  
>.....pTUB1.....>

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6361 ccccttcctt ctctttgcga gtctcgtaga gaacaagcac tcgttcgccg tccctgacga
>.....pTUB1.....>

6421 cgcaaccgc gcagaagaca tccaccaaac ggtgttacac aatcaccttg tgtgaagttc
>.....pTUB1.....>

                                     BglII
                                     -----
6481 ttgcgaaaa ctactcgttg gcattttttc ttgaattccc agatctaaaa tggtagagcaa
>.....pTUB1.....>>
                                     >>.YFP CDS.>
                                     >>>>

6541 gggcgaggag ctgttcaccg ggggtgtgcc catcctggtc gagctggacg gcgacgtaaa
>.....YFP CDS.....>

6601 cggccacaag ttcagcgtgt cgggcgaggg cgagggcgat gccacctacg gcaagctgac
>.....YFP CDS.....>

6661 cctgaagttc atctgcacca ccggcaagct gcccggtccc tggcccaccc tcgtgaccac
>.....YFP CDS.....>
                                     PstI
                                     -----
6721 cttcggctac ggcctgcagt gcttcgcccg ctaccccgac cacatgaagc agcacgactt
>.....YFP CDS.....>

6781 cttcaagtcc gccatgcccg aaggctacgt ccaggagcgc accatcttct tcaaggacga
>.....YFP CDS.....>

6841 cggcaactac aagaccgcg ccgaggtgaa gttcgagggc gacaccctgg ygaaccgcat
>.....YFP CDS.....>

6901 cgagctgaag ggcacgact tcaaggagga cggcaacatc ctggggcaca agctggagta
>.....YFP CDS.....>

6961 caactacaac agccacaacg tctatatcat ggccgacaag cagaagaacg gcatcaaggt
>.....YFP CDS.....>

7021 gaacttcaag atccgccaca acatcgagga cggcagcgtg cagctcgccg accactacca
>.....YFP CDS.....>

7081 gcagaacacc cccatcggcg acggccccgt gctgctgccc gacaaccact acctgagcta
>.....YFP CDS.....>

7141 ccagtccgcc ctgagcaaag accccaacga gaagcgcgat cacatggtcc tgctggagtt
>.....YFP CDS.....>
                                     AvrII
                                     -----
7201 cgtgaccgcc gccgggatca ctctcgcat ggacgagctg tacaagccta ggatgtctag
>.....YFP CDS.....>>
                                     >>.....>
                                     >>>

7261 attagataaa agtaaagtga ttaacagcgc attagagctg cttaatgagg tcggaatcga
>.....TR CDS.....>

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7321 aggtttaaca acccgtaaac tcgcccagaa gctaggtgta gagcagccta cattgtattg
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7381 gcatgtaaaa aataagcggg ctttgctcga cgccttagcc attgagatgt tagataggca
>.....TR CDS.....>

7441 ccatactcac ttttgccctt tagaagggga aagctggcaa gattttttac gtaataacgc
>.....TR CDS.....>

7501 taaaagtttt agatgtgctt tactaagtca tcgcatgga gcaaaagtac atttaggtac
>.....TR CDS.....>

7561 acggcctaca gaaaaacagt atgaaactct cgaaaatcaa ttagcctttt tatgccaaca
>.....TR CDS.....>

7621 aggtttttca ctagagaatg cattatatgc actcagcgt gtggggcatt ttactttagg
>.....TR CDS.....>

7681 ttgcgtattg gaagatcaag agcatcaagt cgctaaagaa gaaagggaaa cacctactac
>.....TR CDS.....>

7741 tgatagtatg cggccattat tacgacaagc tatcgaatta ttgatcacc aaggtgcaga
>.....TR CDS.....>

7801 gccagccttc ttattcggcc ttgaattgat catatgcgga ttagaaaaac aacttaaag
>.....TR CDS.....>
      PstI
      -----
7861 tgaaagtggg tcttaactgc agccacaga agctgcccgt ctctcgttt cctctctttt
>....TR CDS....>
                                >>.....DHFR.....>

7921 cggagggatc agggagatg cctcgggtcg gagagagctg acgagggggt gccagagacc
>.....DHFR.....>

7981 cctgtgtcct ttatcgaaga aaaggatga ctcttcattg ggcatctcac acagtctcac
>.....DHFR.....>

8041 ctgccttgt tttctttttg tcaatcagaa cgaaagcgag ttgcgggtga cgcagatgtg
>.....DHFR.....>

8101 cgtgtatcca ctctgaatg cgttatcgtt ctgtatgccg ctagagtgtt ggactgttgc
>.....DHFR.....>

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>.....DHFR.....>

8221 acgacggaga gaaaggagca ccctctcagt ttccctacga tgtgctgtca gtttcgactc
>.....DHFR.....>

8281 ttcaccgcga acgattggcg atacgtctct gttgacttgt taggctccga ccacgaagct
>.....DHFR.....>

```



<<...T7...<

Figure 1 B

**TubYFP/TR-sagCAT**Molecule Features:

Type	Start	End	Name	Description
GENE	2172	2192	T3	T3 primer for sequencing
REGION	2271	2580	pSAG1	SAG1 5' region including promoter
REGION	2581	2583	SAG1 ATG-I	first ATG
GENE	2581	2634	SAG1 CDS	SAG1 coding sequence
REGION	2632	2634	SAG1 ATG-II	second ATG
GENE	2638	3294	CAT CDS	chloramphenicol acetyl transferase coding sequence
REGION	3295	3607	SAG1-I	SAG1 3' untranslated region
REGION	3614	3747	SAG1-II	repeated part of 3' untranslated region used to start tub promoter
REGION	3748	3799	vector	part of unknown vector
REGION	3800	6520	pTUB1	TUB1 5' region including promoter
GENE	6530	7246	YFP CDS	Yellow fluorescent protein coding sequence
REGION	6530	6532	YFP ATG-I	first ATG
GENE	7253	7876	TR CDS	Tet repressor coding sequence
REGION	7253	7255	TR ATG-I	first ATG
REGION	7886	8656	DHFR	DHFR 3' untranslated region
GENE	8710	8690	C T7	T7 primer for sequencing

Figure 1 C

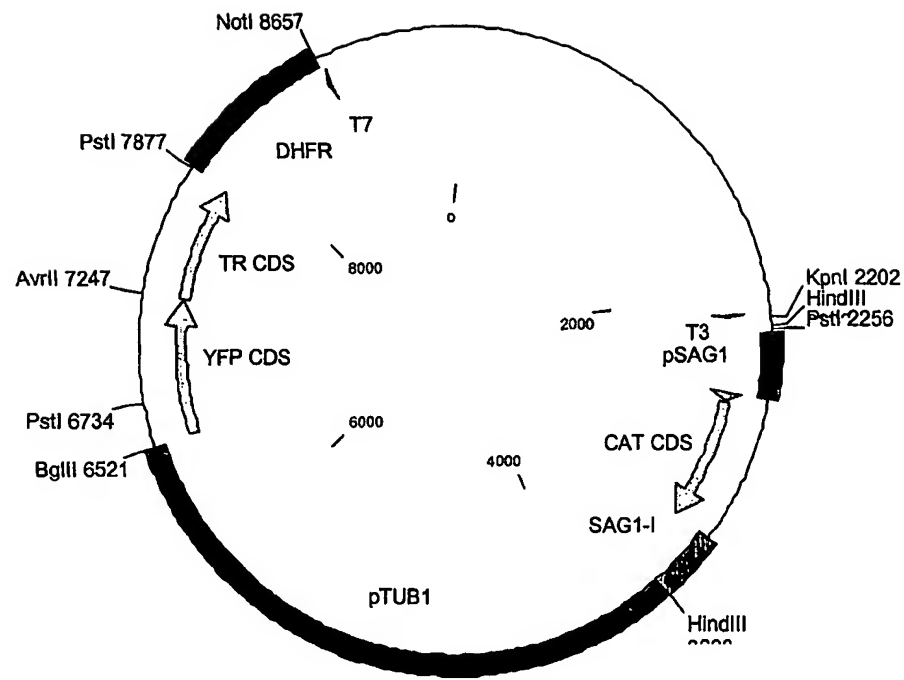
**ptub<sup>YFP</sup>TR<sub>sag</sub>CAT****9332 bp**

Figure 2 A

```
1  agcttcctcg cagagattgt cagtgcattga cacaaccgcg aaaagccggc agccgcggta
   >.....'promoter.....>

61  atacggggac gaggaaaacg actgagcgtc acaacagaag cagccgagta aacggcgaag
   >.....'promoter.....>

121 gaaatggaaa ggacccaagt aaaatttctt gaagaatttc agcgaacaa ctctgcgggt
   >.....'promoter.....>

181 tcttgcaat agaggaattt cacttctca tcgtctgatt tatgcttca tcctctgccg
   >.....'promoter.....>

241 ctcaacagcc gaataaacgg ttctcggtcg ctctctaaa ctctacttca gtagtgtgaa
   >.....'promoter.....>

301 ctcttttgct tcacgagcct tcgtctcagc cctcaccgtc ctgagttctg tctttgttga
   >.....'promoter.....>

361 ggaaagctcc cgctgaaaaa acaggacttt gtttgcagat tttcatgtgt actggaaagt
   >.....'promoter.....>

421 gagatgtgac ttggggaagt ccgctttaaa atttcattg ttttctcaa atgaaaagtc
   >.....'promoter.....>

                                     PstI
                                     -----
481 taaaaaatcg aagtgcgtgc cccgcgagga attccctct gcagatttgt tttgcattta
   >.....'promoter.....>

541 tatgtcgttt ttacggagaa aagtcceaag ctgctgctcc ttctctaact agatgttgaa
   >.....'promoter.....>

601 cgctagcaca tatgcaccag atgcttctga agtataccta aacgcacctt gggaacaact
   >.....'promoter.....>

661 gtgctcccat tcataaaact catacaagtc accaagcatg ccataccgtg gagacataac
   >.....'promoter.....>

721 aacggaagct agactactcc cccctgttat tgcacactat cgaaaaggat tcctaggttt
   >.....'promoter.....>

                                     PstI
                                     -----
781 ctatcctctg ccttttctcg gggcacactg cagagaaact accgtgcgcg ctacctcccg
   >.....'promoter.....>

841 acgtgcgagg cgatagcaaa acgcttttga aggaaaaagt cgagaaatcg acgactgcgt
   >.....'promoter.....>
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901 ctcttgaatc cgagagaggg atccaaccca ccgagttctc tgcattgtgca gcattctgcaa  
>.....'promoter.....>

961 gaacgtgata atgcatgaac tcgattcatcg ccttatctgt gtgcatgcat ttctgaaaaa  
>.....'promoter.....>

1021 gaaaggcggtt ttctgcgcg agactcgcg ggaggcaaga cgagactttc tcctcttcca  
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1081 aactgcgagc cacgggggcg catgcaattt gaacatcacg caaaatccca aaacgggtgg  
>.....'promoter.....>

1141 ggtggagccg caaacttttt tggcatgcag cgttgagcct gagctcggtt gggggctttt  
>.....'promoter.....>

1201 gtcgagagcg tggggtgccc cgagagagca acgcggcgt acgcgccga cgggtcttct  
>.....'promoter.....>

1261 gggaagcctc gcatttcctc gacgggttct cccctcaatt ctcttcctt ctctgcgtct  
>.....'promoter.....>>  
>>.....e.....>

1321 tcctcaggtg gcttcgtcac cggtttttct cctcggttc gtgctccgt gtgtgtccg  
>.....e.....>

1381 agtgccgca cagatcgagg gcgttctccg ctccacctt gcggttccca atttcgattt  
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1441 ttctccgtca ccatggggcg catgtacgtt cctggaaagg gcattgtctc ctctaggatg  
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>>>  
>>.....cds.....>>  
>>...>

1501 accatgatta cggattcact ggccgtcgtt ttacaacgtc gtgactggga aaacctggc  
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1561 gttaccaaac ttaatgcct tgcagcacat ccccttttcg ccagctggcg taatagcgaa  
>.....'LacZ.....>

1621 gagggccgca ccgattcgcc ttccaacag ttgcgcagcc tgaatggcg atggcgctt  
>.....'LacZ.....>

1681 gcctggtttc cggcaccaga agcggtgccg gaaagctggc tggagtgcga tcttcctgag  
>.....'LacZ.....>

1741 gccgatactg tcgtcgccc ctcaaactgg cagatgcacg gttacgatgc gcccatctac  
>.....'LacZ.....>

1801 accaacgtga cctatcccat tacggtcaat ccgccgttg ttccacgga gaatccgacg  
>.....'LacZ.....>

1861 gggtgttact cgctcacatt taatgttgat gaaagctggc tacaggaagg ccagacgcga  
>.....'LacZ.....>

1921 attatTTTTg atggcgtaa ctgcgcgtt catctgtgt gcaacggcg ctgggtcgt  
>.....'LacZ.....>

1981 tacggccagg acagtcgtt gccgtctgaa ttgacctga gcgcattttt acgcgccga  
>.....'LacZ.....>

2041 gaaaaccgcc tcgcggtgat ggtgctgcgc tggagtgcg gcagttatct ggaagatcag  
>.....'LacZ.....>

2101 gatatgtggc ggatgagcgg cttttccgt gacgtctcgt tgctgcataa accgactaca  
>.....'LacZ.....>

2161 caaatcagcg atttccatgt tgccactcgc tttaatgatg atttcagccg cgctgtactg  
>.....'LacZ.....>

2221 gaggtgaag ttcagatgtg cggcgagttg cgtgactacc tacgggtaac agtttcttta  
>.....'LacZ.....>

2281 tggcagggtg aaacgcaggt cgcagcggc accgcgcctt tcggcgggta aattatcgat  
>.....'LacZ.....>

2341 gagcgtggtg gttatgccga tcgcgtcaca ctacgtctga acgtcgaaaa cccgaaactg  
>.....'LacZ.....>

2401 tggagcgccg aaatcccgaa tctctatcgt gcggtggtg aactgcacac cgcgcagcg  
>.....'LacZ.....>

2461 acgctgattg aagcagaagc ctgcgatgtc ggtttcccg aggtgcggat tgaatatggt  
>.....'LacZ.....>

2521 ctgctgctgc tgaacggcaa gccgttgctg attcgaggcg ttaaccgtca cgagcatcat  
>.....'LacZ.....>

2581 cctctgcatg gtcaggatcat ggatgagcag acgatggtgc aggatatcct gctgatgaag  
>.....'LacZ.....>

2641 cagaacaact ttaacgccgt gcgctgttcg cattatccga accatccgct gtggtacacg  
>.....'LacZ.....>

2701 ctgtgcgacc gctacggcct gtatgtggtg gatgaagcca atattgaaac ccacggcatg  
>.....'LacZ.....>

2761 gtgccaatga atcgtctgac cgatgatccg cgctggctac cggcgatgag cgaacgcgta  
>.....'LacZ.....>

2821 acgcgaatgg tgcagcgca tcgtaatcac ccgagtgtga tcctctggtc gctggggaat  
>.....'LacZ.....>

2881 gaatcaggcc acggcgctaa tcacgacgcg ctgtatcgct ggatcaaacc tgcgatcct  
>.....'LacZ.....>

2941 tcccgcccg tgcagtatga aggcggcgga gccgacacca cggccaccga tattatttgc  
>.....'LacZ.....>

3001 ccgatgtacg cgcgcgtgga tgaagaccag cccttcccgg ctgtgccgaa atggtccatc  
>.....'LacZ.....>

3061 aaaaaatggc ttctgctacc tggagagacg cgcgcgtga tcctttgcga atacgccac  
>.....'LacZ.....>

3121 gcgatgggta acagtcttgg cggtttcgct aaatactggc aggcgtttcg tcagtatccc  
>.....'LacZ.....>

3181 cgtttacagg gcggcttcgt ctgggactgg gtggatcagt cgctgattaa atatgatgaa  
>.....'LacZ.....>

3241 aacggcaacc cgtggtcggc ttacggcggg gatcttggcg atacgccgaa cgatcgccag  
>.....'LacZ.....>

3301 ttctgtatga acggtctggt ctttgcgcac cgcacgccgc atccagcgct gacggaagca  
>.....'LacZ.....>

3361 aaacaccagc agcagttttt ccagttccgt ttatccgggc aaaccatcga agtgaccagc  
>.....'LacZ.....>

3421 gaatacctgt tccgtcatag cgataacgag ctctgcact ggatgggtggc gctggatggt  
>.....'LacZ.....>

3481 aagccgctgg caagcgggta agtgctctg gatgtcgtc cacaaggtaa acagttgatt  
>.....'LacZ.....>

3541 gaactgcctg aactaccgca gccggagagc gccgggcaac tctggctcac agtacgcgta  
>.....'LacZ.....>

3601 gtgcaaccga acgcgaccgc atggtcagaa gccgggcaca tcagcgctg gcagcagtg  
>.....'LacZ.....>

3661 cgtctggcgg aaaacctcag tgtgacgtc ccgcgcgct ccacgccat ccgcacctg  
>.....'LacZ.....>

3721 accaccagc aaatggattt ttgcatcgag ctgggtaata agcgttgga atttaaccgc  
>.....'LacZ.....>

3781 cagtcaggct ttctttcaca gatgtggatt ggcgataaaa aacaactgct gacgccgctg  
>.....'LacZ.....>

3841 cgcgatcagt tcacccgtgc accgctggat aacgacattg gcgtaagtga agcgaccgc  
>.....'LacZ.....>

```

3901 attgacccta acgcctgggt cgaacgctgg aaggcggcgg gccattacca gcccgaagca
>.....'LacZ.....>

3961 gcgttggtgc agtgcacggc agatacactt gctgatgcgg tgctgattac gaccgctcac
>.....'LacZ.....>

4021 gcgtggcagc atcaggggaa aaccttattt atcagccgga aaacctaccg gattgatggt
>.....'LacZ.....>

4081 agtggcaaa tggcgattac cgttgatggt gaagtggcga gcgatacacc gcatccggcg
>.....'LacZ.....>

4141 cggattggcc tgaactgcc a gctggcgcag gtagcagagc gggtaaactg gctcggatta
>.....'LacZ.....>

4201 gggccgcaag aaaactatcc cgaccgcctt actgccgcct gttttgaccg ctgggatctg
>.....'LacZ.....>

4261 ccattgtcag acatgtatac cccgtacgtc ttcccgagcg aaaacggctc gcgctgcggg
>.....'LacZ.....>

4321 acgcgcgaat tgaattatgg cccacaccag tggcgcgggc acttccagtt caacatcagc
>.....'LacZ.....>

4381 cgctacagtc aacagcaact gatggaaacc agccatcgcc atctgctgca cgcggaagaa
>.....'LacZ.....>

4441 ggcacatggc tgaatatcga cggtttccat atggggattg gtggcgacga ctctgggagc
>.....'LacZ.....>

4501 ccgtcagtat cggcggaatt ccagctgagc gccggtcgct accattacca gttggtctgg
>.....'LacZ.....>

          PstI
          -----
4561 tgtcaaaaat aactgcagcc cacagaagct gcccgctctc cgttttcctc tcttttcgga
>.....'LacZ.....>>
          >>.....DHFR .....>

4621 gggatcaggg agagtgcctc gggtcggaga gagctgacga gggggtgcc gagacccctg
>.....DHFR .....>

4681 tgtcctttat cgaagaaaag ggatgactct tcatgtggca ttccacacag tctcacctcg
>.....DHFR .....>

4741 ccttgttttc tttttgtcaa tcagaacgaa agcgagttgc gggtgacga gatgtgcgtg
>.....DHFR .....>

4801 tatccactcg tgaatgcgtt atcgttctgt atgccgctag agtgctggac tgttgctgtc
>.....DHFR .....>

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4861  tgcccacgac agcagacaac tttccttcta tgcacttgca ggatggtgca gcgcaaacga
>.....DHFR .....>

4921  cggagagaaa ggagcaccct ctcagtttcc ctacgatgtg ctgtcagttt cgactcttca
>.....DHFR .....>

4981  ccgcgaacga ttggcgatac gtctctgttg acttggttagg ctccgaccac gaagctccct
>.....DHFR .....>

5041  taactarata agccgcgaca cctaagtgtg caccatttgc agatcgataa tctgcgaccg
>.....DHFR .....>

5101  ctgaatccgt ccagatcagt aaaaccgcac cacctaagtg taaaccttgt ttaggtcgat
>.....DHFR .....>

5161  aaaatgctac caacccccac ccacaatcga gccttgagcg tttctgcgca cgcgttggcc
>.....DHFR .....>

5221  tacgtgactt gctgatgcct gcctctggcc attcatgcca gtcagtgcgc ataaaaatgt
>.....DHFR .....>

5281  ggacacagtc ggttgacaag tgttctggca ggctacagtg acaccgcggt ggagggggat
>.....DHFR .....>

                                NotI
                                -----
5341  ccactagttc tagagcggcc gccaccgcgg tggagctcca attcgcccta tagtgagtcg
>...DHFR ....>>
                                <<....T7.....<

5401  tattacgcgc gtcactggc cgtcgtttta caacgctgtg actgggaaaa ccctggcggt
<.T7..<<
>>.....pKS+.....>

5461  acccaactta atcgcccttc agcacatccc ctttgcgcca gctggcgtaa tagcgaagag
>.....pKS+.....>

5521  gcccgcacgc atcgcccttc ccaacagttg cgcagcctga atggcgaatg ggacgcgccc
>.....pKS+.....>

5581  tgtagcggcg cattaagcgc ggcgggtgtg gtggttacgc gcagcgtgac cgctacactt
>.....pKS+.....>

5641  gccagcgccc tagcgccgcg tcctttcgct ttcttccctt cctttctcgc caggttcgcc
>.....pKS+.....>

5701  ggctttcccc gtcaagctct aaatcggggg ctcccttttag ggttccgatt tagtgcttta
>.....pKS+.....>

5761  cggcacctcg accccaaaaa acttgattag ggtgatgggt cacgtagtgg gccatcgccc
>.....pKS+.....>

```

5821 tgatagacgg tttttcgccc tttagcgttg gagtcacgt tctttaatag tggactcttg  
>.....pKS+.....>

5881 ttccaaactg gaacaacact caaccctatc tcggtctatt cttttgattt ataagggatt  
>.....pKS+.....>

5941 ttgccgattt cggcctattg gttaaaaaat gagctgattt aacaaaaatt taacgcgaat  
>.....pKS+.....>

6001 ttttaaaaaa tattaacgct tacaatttag gtggcacttt tcggggaaat gtgcgcggaa  
>.....pKS+.....>

6061 cccctatttg tttatttttc taaatacatt caaatatgta tccgctcatg agacaataac  
>.....pKS+.....>

6121 cctgataaat gcttcaataa tattgaaaaa ggaagagtat gagtattcaa catttccttg  
>.....pKS+.....>

6181 tcgcccttat tccctttttt gcggcatttt gccttcctgt ttttgctcac ccagaaacgc  
>.....pKS+.....>

6241 tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg agtgggttac atcgaactgg  
>.....pKS+.....>

6301 atctcaacag cggtaagatc cttgagagtt ttcccccga agaactttt ccaatgatga  
>.....pKS+.....>

6361 gcacttttaa agttctgcta tgtggcgagg tattatcccg tattgacgcc gggcaagagc  
>.....pKS+.....>

6421 aactcggctg ccgcatacac tattctcaga atgacttggg tgagtactca ccagtcacag  
>.....pKS+.....>

6481 aaaagcatct tacggatggc atgacagtaa gagaattatg cagtgcctgcc ataaccatga  
>.....pKS+.....>

6541 gtgataacac tgcggccaac ttacttctga caacgatcgg aggaccgaag gagctaaccg  
>.....pKS+.....>

6601 cttttttgca caacatgggg gatcatgtaa ctgccttga tcgttgggaa ccggagctga  
>.....pKS+.....>

6661 atgaagccat accaaaacgac gagcgtgaca ccacgatgcc tntagcaatg gcaacaacgt  
>.....pKS+.....>

6721 tgcgcaaact attactggc gaactactta ctctagcttc ccggcaacaa ttaatagact  
>.....pKS+.....>

6781 ggatggaggc ggataaagtt gcaggaccac ttctgcgctc ggcccttccg gctggctggg  
>.....pKS+.....>

6841 ttattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt gcagcactgg  
>.....PKS+.....>

6901 ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt caggcaacta  
>.....PKS+.....>

6961 tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag cattggtaac  
>.....PKS+.....>

7021 tgtcagacca agtttactca tatatacttt agattgattt aaaacttcat ttttaattta  
>.....PKS+.....>

7081 aaaggatcta ggtgaagatc ctttttgata atctcatgac caaaatccct taacgtgagt  
>.....PKS+.....>

7141 tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa aggatcttct tgagatcctt  
>.....PKS+.....>

7201 tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc accgctacca gcggtggttt  
>.....PKS+.....>

7261 gtttgccgga tcaagagcta ccaactcttt ttccgaaggt aactggcttc agcagagcgc  
>.....PKS+.....>

7321 agataccaaa tactgtcctt ctagtgtagc cgtagttagg ccaccacttc aagaactctg  
>.....PKS+.....>

7381 tagcaccgcc tacatacctc gctctgctaa tcctgttacc agtggctgct gccagtggcg  
>.....PKS+.....>

7441 ataagtcgtg tcttaccggg ttggactcaa gacgatagtt accggataag gcgcagcggg  
>.....PKS+.....>

7501 cgggctgaac ggggggttcg tgcacacagc ccagcttggg gcgaacgacc tacaccgaac  
>.....PKS+.....>

7561 tgagatacct acagcgtgag ctatgagaaa gcgccacgct tcccgaaggg agaaaggcgg  
>.....PKS+.....>

7621 acaggatatcc ggtaagcggc agggtcggaa caggagagcg cacgaggag cttccagggg  
>.....PKS+.....>

7681 gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca cctctgactt gagcgtcgat  
>.....PKS+.....>

7741 ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa cgccagcaac gcggcctttt  
>.....PKS+.....>

7801 tacggttcct ggccttttgc tggccttttg ctcacatggt ctttcctgcg ttatcccctg  
>.....PKS+.....>

```
7861 attctgtgga taaccgtatt accgcctttg agtgagctga taccgctcgc cgcagccgaa
>.....PKS+.....>

7921 cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga gcgcccaata cgcaaaccgc
>.....PKS+.....>

7981 ctctccccgc gcgttggcgc attcattaat gcagctggca cgacaggttt cccgactgga
>.....PKS+.....>

8041 aagcgggcag tgagcgcaac gcaattaatg tgagttagct cactcattag gcaccccagg
>.....PKS+.....>

8101 ctttacactt tatgcttcgc gctcgtatgt tgtgtggaat tgtgagcgga taacaatttc
>.....PKS+.....>

8161 acacaggaaa cagctatgac catgattacg ccaagcgcg cattaaccct cactaaaggg
>.....PKS+.....>>
>>.....T3 .....>

          KpnI                      HindIII
          -----                      -----
8221 aacaaaagct gggtaccggg ccccccctcg aggtcgacgg tatcgata
>>
```

Figure 2 B

Molecule: S13/lacZ, 8268 bps DNA Circular

## Molecule Features:

Type	Start	End	Name	Description
REGION	1	1294	'promoter	promoterregion
REGION	1295	1492	e	exon 1
REGION	1453	1455	atg	ATG start
GENE	1453	1492	cds	gen
GENE	1495	4578	'LacZ	LacZ gene from E.coli BL21
REGION	4582	5354	DHFR	DHFR 3' untranslated region
GENE	5408	5388 C	T7	T7 primer for sequencing
REGION	5408	8202	pKS+	pKS+ vector
GENE	8202	8222	T3	T3 primer for sequencing

Figure 2 C

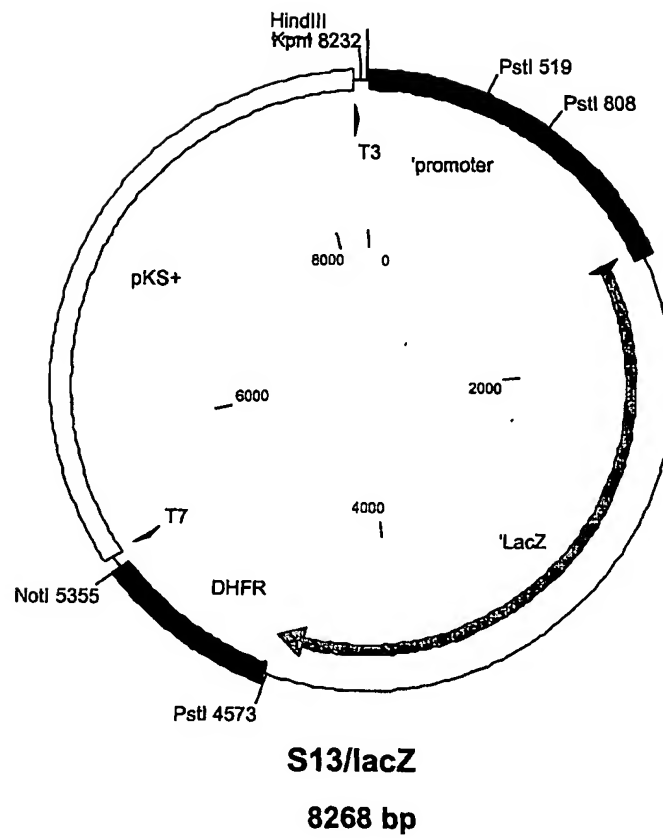


Figure 3 A

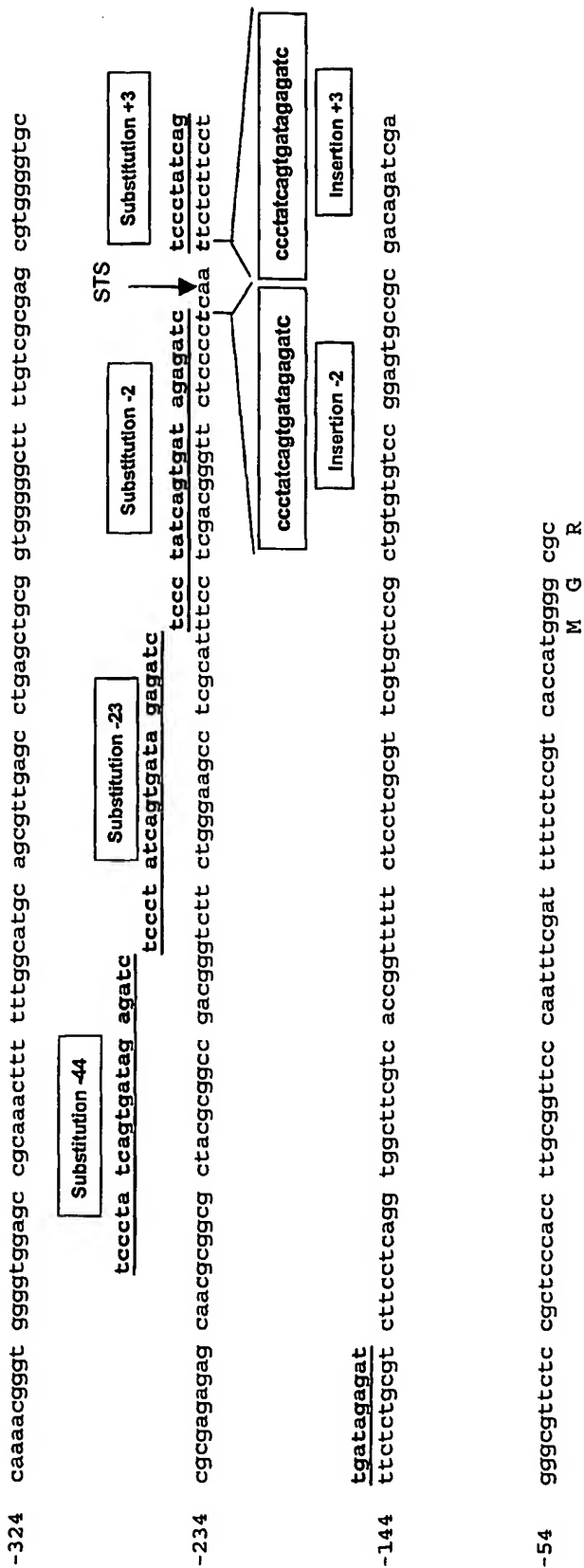


Figure 3 B

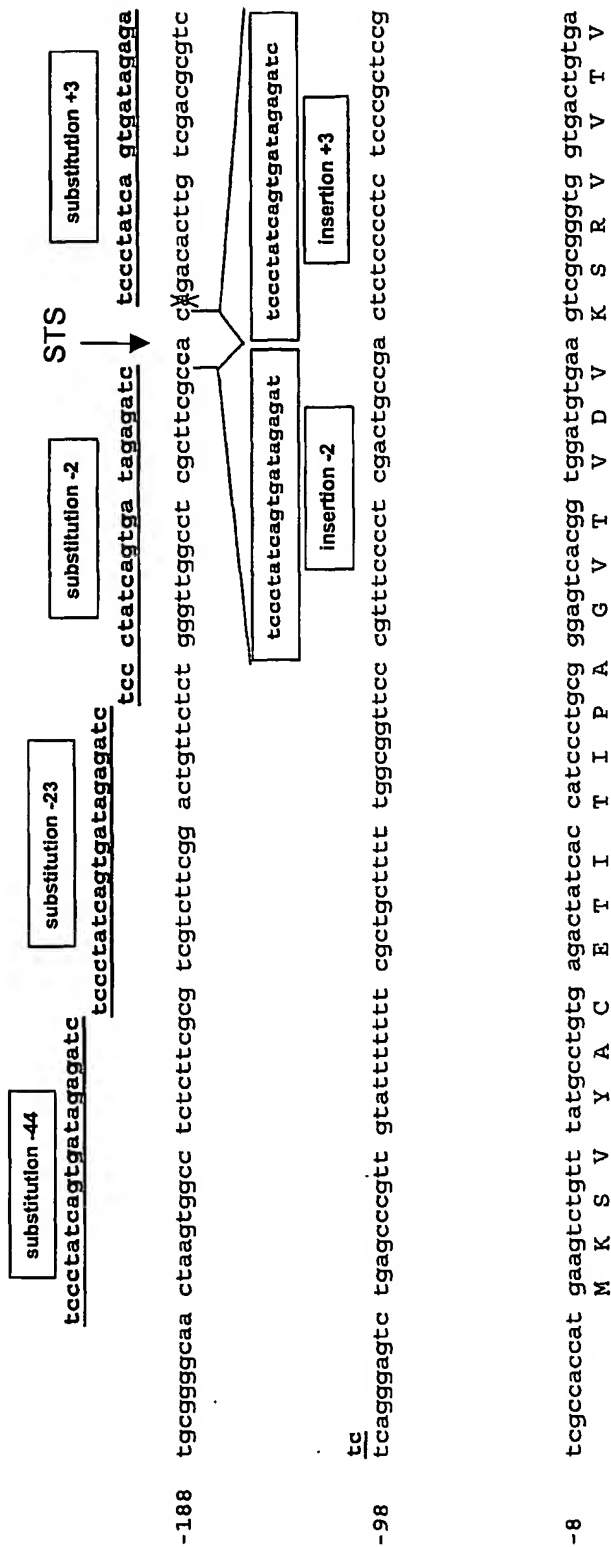




Figure 4

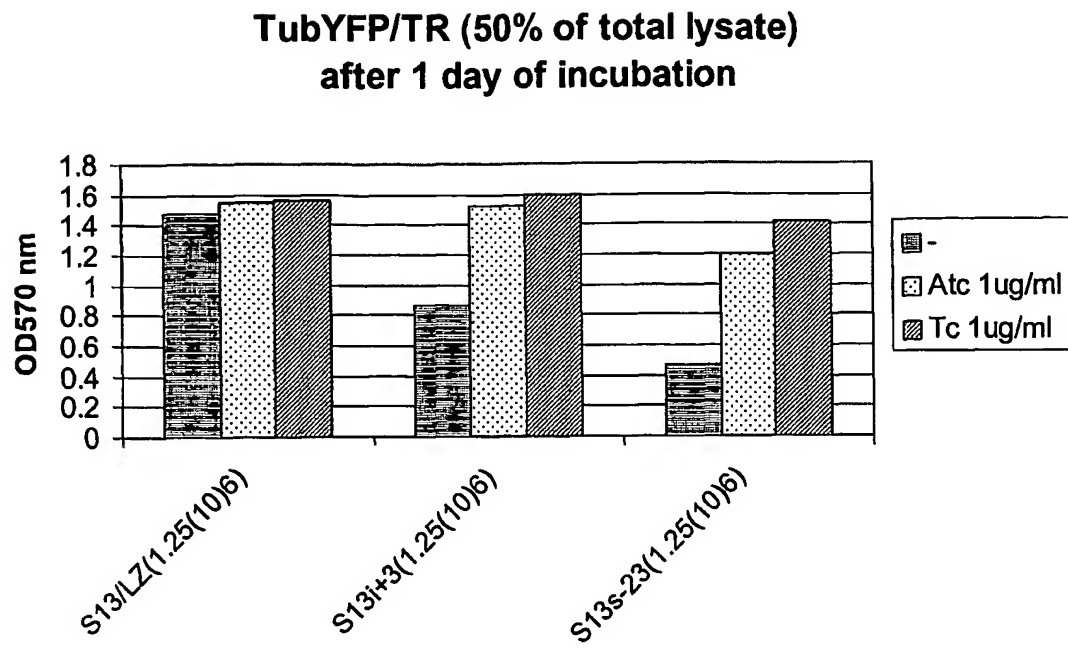


Figure 5

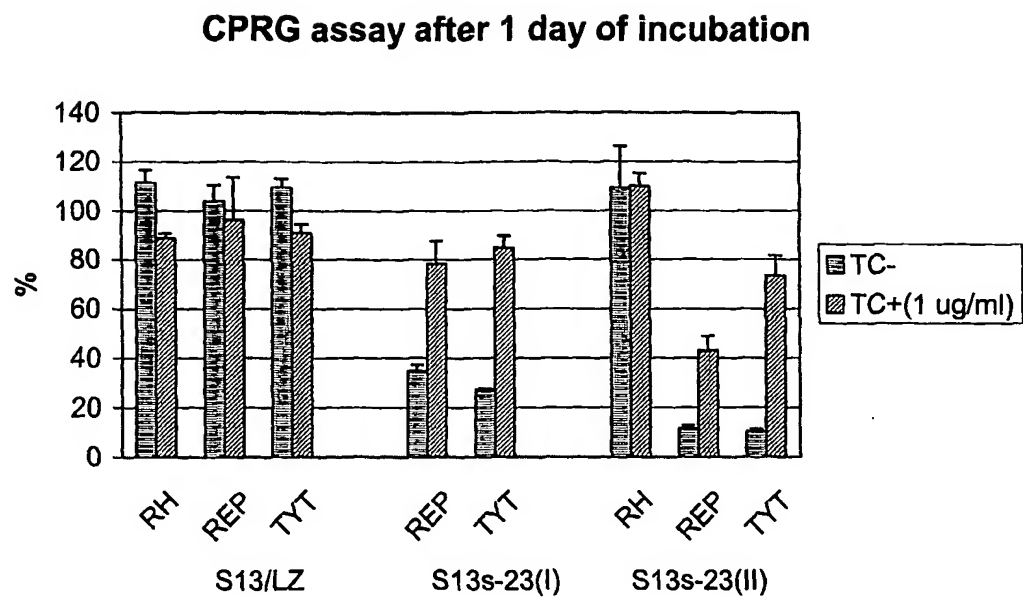


Figure 6

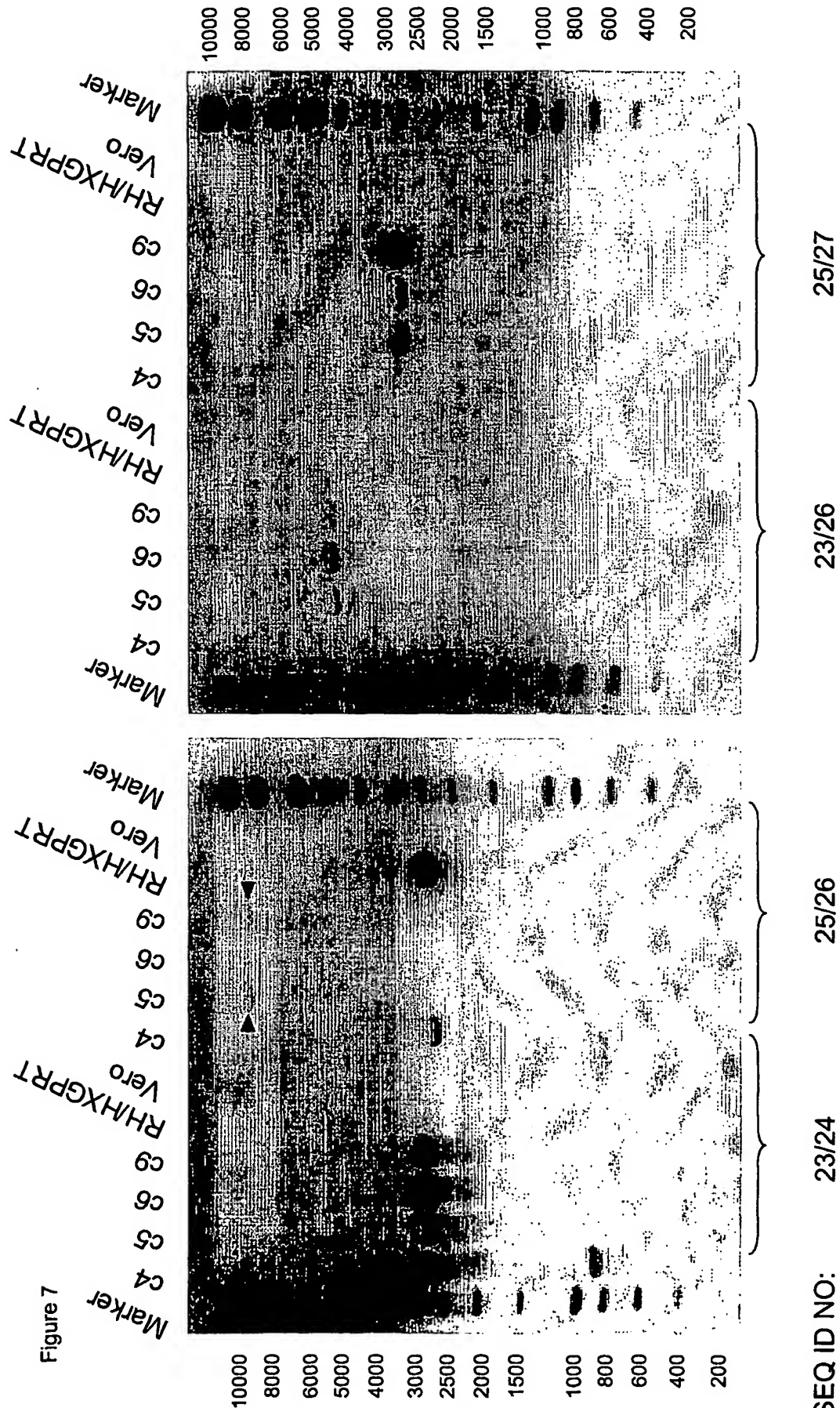


Figure 7